# Genome-scale metabolic model of Pichia pastoris with native and humanized glycosylation of recombinant proteins - DTU Orbit (08/11/2017)

**Genome-scale metabolic model of *Pichia pastoris* with native and humanized glycosylation of recombinant proteins**

*Pichia pastoris* is used for commercial production of human therapeutic proteins, and genome-scale models of *P. pastoris* metabolism have been generated in the past to study the metabolism and associated protein production by this yeast. A major challenge with clinical usage of recombinant proteins produced by *P. pastoris* is the difference in N-glycosylation of proteins produced by humans and this yeast. However, through metabolic engineering, a P. pastoris strain capable of producing humanized N-glycosylated proteins was constructed. The current genome-scale models of *P. pastoris* do not address native nor humanized N-glycosylation, and we therefore developed ihGlycopastoris, an extension to the iLC915 model with both native and humanized N-glycosylation for recombinant protein production, but also an estimation of N-glycosylation of *P. pastoris* native proteins. This new model gives a better prediction of protein yield, demonstrates the effect of the different types of N-glycosylation of protein yield, and can be used to predict potential targets for strain improvement. The model represents a step towards a more complete description of protein production in *P. pastoris*, which is required for using these models to understand and optimize protein production processes.

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